

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: January 31, 2005, 18:10:30 i Search time 20 Seconds  
(without alignments)  
48.108 Million cell updates/sec

Title: US-10-083-768-5  
Perfect score: 25  
Sequence: 1 XXGXXXXWX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database :

PIR79+:  
1: pir1,\*  
2: pir2,\*  
3: pir3,\*  
4: pir4,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	68.0	72	H90603	hypothetical prote
2	17	68.0	132	2	hypothetical 14.2K prote
3	17	68.0	165	2	hypothetical 14.2K prote
4	17	68.0	203	2	hypothetical prote
5	17	68.0	239	2	hypothetical prote
6	17	68.0	251	2	NADH-Flavin Oxido
7	17	68.0	272	2	hypothetical prote
8	17	68.0	297	2	probable sugar up
9	17	68.0	308	2	hypothetical prote
10	17	68.0	406	2	acetamidase - Myco
11	17	68.0	408	2	hypothetical prote
12	17	68.0	408	2	probable PAD-linker
13	17	68.0	433	2	hypothetical prote
14	17	68.0	492	2	hemolysin - Aeromo
15	17	68.0	523	2	probable secretory
16	17	68.0	547	2	hypothetical prote
17	17	68.0	579	2	probable secretory
18	17	68.0	624	2	alpha-galactosidases
19	17	68.0	735	2	conserved hypothetical
20	17	68.0	776	1	outer layer protei
21	17	68.0	776	1	outer layer protei
22	17	68.0	776	1	outer layer protei
23	17	68.0	776	1	outer layer protei
24	17	68.0	776	1	outer layer protei
25	17	68.0	776	1	outer layer protei
26	17	68.0	776	1	outer layer protei
27	17	68.0	776	1	outer layer protei
28	17	68.0	776	2	outer capsid protei
29	17	68.0	776	2	outer layer protei

## ALIGNMENTS

RESULT 1  
H90603  
hypothetical protein MYPU\_7360 [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)  
C;Species: *Mycoplasma pulmonis*  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: H90603  
R;Chambard, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
Nucleic Acids Res, 29, 2145-2153, 2001  
A;Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulmo-*  
A;Reference number: A99312; MUID:21267165; PMID:11353084  
A;Accession: H90603  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-72 <KUR>  
A;Cross-references: UNIPROT:Q98P16; GB:AL445566; PID:914090151; PIDN:CAC13909-1; GSPPDB:G  
C;Genetics:  
A;Gene: MYPU\_7360  
A;Genetic code: SGCG3

Query Match 68.0%; Score 17; DB 2; Length 72;  
Best Local Similarity 28.6%; Pred. No. 8.6e+02;  
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 GXXXXXW 9  
Db 39 GAATSW 45

RESULT 2  
C41855  
hypothetical 14.2K beta-lactamase regulatory protein - *Streptomyces cacaoi*  
C;Species: *Streptomyces cacaoi*  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: C41855  
R;Drabe, H.; Ogawara, H.  
J. Bacteriol. 174: 2834-2842, 1992  
A;Title: Nucleotide sequence and transcriptional analysis of activator-regulator protein  
A;Reference number: A41855; MUID:92234939; PMID:1569015  
A;Accession: C41855  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-132 <URA>  
A;Cross-references: UNIPROT:P33554; GB:D00937; PID:9216997; PID:9210776-1; PID:9217001  
A;Note: Sequence extracted from NCBI backbone (NCBIN:97018, NCBI:97029)  
C;Superfamily: *Streptomyces cacaoi* hypothetical 14.2K beta-lactamase regulatory protein

Query Match 68.0%; Score 17; DB 2; Length 132;  
Best Local Similarity 28.6%; Pred. No. 1.4e+03;  
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 3 GXXXXXW 9

Db 53 GSSASSW 59

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-239 <SEE>

A;Cross-references: UNIPROT:Q9S1Z1; EMBL:AU109747; PIDN:CAH52362.1; GSPDB:GR00070; SCOED

A;Experimental source: strain A3 (2)

C;Genetics: SCOEDB:SCJ21.16

Query Match 68.0%; Score 17; DB 2; Length 239;

Best Local Similarity 28.6%; Pred. No. 2.3e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXW 9

Db 172 GSSAAW 178

RESULT 6

AB0119 NADPH-Flavin oxidoreductase BH2953 [imported] - *Bacillus halodurans* (strain C-125)

C;Species: *Bacillus halodurans*

C;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; GB:BA000004; PIDN:910175500; PIDN:BAB066:

C;Accession: AB0119 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirai

Nucleic Acids Res. 28, 431-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its

A;Reference number: A83650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; GB:BA000004; PIDN:910175500; PIDN:BAB066:

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXW 9

Db 211 GATTTW 217

RESULT 7

T15820 hypothetical protein C52B11.2 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Accession: T15820 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C;Accession: T15820

R;Martin, J.

submitted to the EMBL Data Library, November 1995

A;Description: The sequence of *C. elegans* cosmid C52B11.

A;Reference number: Z18411

A;Accession: T15820

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-272 <MAR>

A;Cross-references: UNIPROT:Q18776; EMBL:U41276; PIDN:91086884; PIDN:g1086886; PIDN:AAA824c

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:C52B11.2

A;Introns: 12/1; 91/3; 190/3; 221/3

Query Match 68.0%; Score 17; DB 2; Length 272;

Best Local Similarity 28.6%; Pred. No. 2.6e+03;

Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXW 9

Db 77 GSSSSW 83

RESULT 5

T37065 hypothetical protein SCJ21.16 - *Streptomyces coelicolor*

C;Species: *Streptomyces coelicolor*

C;Accession: T37065 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A;Reference number: 221620

A;Accession: T37065

RESULT 8

E96002 probable sugar uptake ABC transporter permease protein SMB21459 [imported] - Sinorhizobi

C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C;Accession: E96002

R;Finan, T.M.; Weidner, S.; Wong, K.; Buijtemer, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1.68-kb pSymB megaplasmid from the N2-fixing endo

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: E6002

A;Status: preliminary

A;Molecule type: DNA; protein

A;Residues: 1-406 <MAH>

A;Cross-references: UNIPROT:Q92U54; GB:AL591985; PIDN:CAC49685.1; PID:915141172; GSPPDB:G

A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Barloy-Hubler, F.; Lelaurae, C.;

peila, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leal, D.;

hebault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Content: annotation

C;Genetics:

A;Gene: SMB21459

C;Superfamily: inner membrane protein uspA

Query Match 68.0%; Score 17; DB 2; Length 297;

Best Local Similarity 28.6%; Pred. No. 2.7e+03; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 GXXXXW 9

Db 268 GAAASTW 274

RESULT 9

B84311 hypothetical protein Vng1578h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Accession: B84311

R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.

; Leithäuser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonka, M.; Alam, M.; Fritas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbhardt, H.; Lowe, T.M.; Li

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: B84311

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-308 <SNP>

A;Cross-references: UNIPROT:Q9HPL3; GB:AE004437; PIDN:AAG19854.1; GSPPDB:G

C;Genetics:

A;Gene: VNG1578H

C;Superfamily: cobalamin biosynthesis protein D

Query Match 68.0%; Score 17; DB 2; Length 308;

Best Local Similarity 28.6%; Pred. No. 2.8e+03; Indels 0; Mismatches 5; Indels 5; Gaps 0;

Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 GXXXXW 9

Db 172 GAAAAAW 178

RESULT 10

H87193 probable PAD-linked oxidoreductase ML2276 [imported] - Mycobacterium leprae

C;Species: Mycobacterium leprae

C;Accession: H87193

R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, R.;

A;Reference number: A86509; MUID:21128732; PMID:1234002

A;Accession: H87193

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:Q9CBA6; GB:AL450380; NID:913093912; PIDN:CA31792.1; GSPDB:G
A;Gene: ML2276

Query Match 68.0%; Score 17; DB 2; Length 408;
Best Local Similarity 28.6%; Pred. No. 3.5e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
A;Residues: 1-408
A;Cross-references: UNIPROT:Q9CBA6; GB:AL450380; NID:913093912; PIDN:CA31792.1; GSPDB:G
C;Genetics:
A;Gene: ML2276

Qy 3 GXXXXXW 9
Db 18 GSAAATW 24

RESULT 13
C69222
hypothetical protein MT9913. - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69222
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Jiwani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noeiling, J.; Reeve, J.N.
J;Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: C69222
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-433 <MPH>
A;Cross-references: UNIPROT:O26998; GB:AE000867; GB:AE000666; NID:g2622009; PIDN:AAB88541
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MRP13
A;Start codon: GTG

Query Match 68.0%; Score 17; DB 2; Length 433;
Best Local Similarity 28.6%; Pred. No. 3.7e+03;
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
A;Residues: 1-433 <MPH>
A;Cross-references: UNIPROT:O26998; GB:AE000867; GB:AE000666; NID:g2622009; PIDN:AAB88541
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MRP13
A;Start codon: GTG

RESULT 14
I39591
hemolysin - Aeromonas hydrophila
N;Alternate names: aerolysin
C;Species: Aeromonas hydrophila
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004
C;Accession: I39591; S26573; S26574
R;Hirono, I.; Aoki, T.; Aiba, T.; Kozaki, S.
Microb. Pathog. 13, 433-446, 1992
A;Title: Nucleotide sequences and characterization of haemolysin genes from Aeromonas hydrophila
A;Reference number: I39590; MUID:93254202; PMID:13022834
A;Accession: I39591
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-492 <RES>
A;Cross-references: UNIPROT:Q06303; EMBL:X65043; NID:938816; PIDN:CAA46179.1; PID:938817
A;Accession: I39590
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-56; 'V' 58-295; 'P' 297-492 <RE2>
A;Cross-references: EMBL:X65044; NID:g38814; PIDN:CAA46180.1; PID:938815
A;Experimental source: strain 28SA
C;Superfamily: aerolysin

Query Match 68.0%; Score 17; DB 2; Length 492;
Best Local Similarity 28.6%; Pred. No. 4.1e+03;

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